

FIG. 1

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Interleukin-22

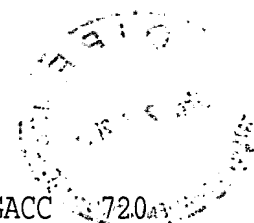
1 GGAATTCGGCACGAGCTCGTGCCGTGCTCAGTGCCTTCCACCACACGCTGCAGCTGGGGC 60
1 N S A R A R A V L S A F H H T L Q L G P 20

61 CGCGTGAGCAGGCGCGCAACGCGAGCTGCCCCGCGAGGGGGCAGGCCCCGCGACCGCCGCT 120
21 R E Q A R N A S C P A G G R P A D R R F 40
121 TCCGGCCGCCACCAACCTGCGCAGCGTGTGCCCCTGGGCCTACAGAATCTCCTACGACC 180
41 R P P T N L R S V S P W A Y R I S Y D P 60
Domain I
181 CGGCGAGGTACCCAGGTACCTGCCTGAAGCCTACTGCCTGTGCCGGGGCTGCCTGACCG 240
61 A R Y P R Y L P E A Y C L C R G C L T G 80
Domain I Domain II
241 GGCTGTTCTGGCGAGGAGGACGTGCGCTTCCGCGAGCGCCCCTGTCTACATGCCACCGTCCG 300
81 L F G E E D V R F R S A P V Y M P T V V 100
Domain III
301 TCCTGCGCCGCACCCCGCCTGCGCCGGCGGCCGTTCCGTCTACACCGAGGCCTACGTCA 360
101 L R R T P A C A G G R S V Y T E A Y V T 120
Domain III

361 CCATCCCCGTGGGCTGCACCTGCGTCCCCGAGCCGGAGAAGGACGCAGACAGCATCAACT 420
121 I P V G C T C V P E P E K D A D S I N S 140
Domain IV
421 CCAGCATCGACAAACAGGGCGCCAAGCTCCTGCTGGGCCCCAACGACGCGCCCGCTGGCC 480
141 S I D K Q G A K L L L G P N D A P A G P 160
481 CCTGAGGCCGGTCTGCCCCGGGAGGTCTCCCCGGCCCGCATCCCAGGGCGCCAAGCTG 540
541 GAGCCGCCTGGAGGGCTCGGTGCGCGACCTCTGAAGAGAGTGCACCGAGCAAACCAAGTG 600
601 CCGGAGCACCAGCGCCGCTTTCCATGGAGACTCGTAAGCAGCTTCATCTGACACGGGCA 660

FIG. 2A

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661 TCCCTGGCTTGCTTTTAGCTACAAGCAAGCAGCGTGGCTGGAAGCTGATGGGAAACGACC 720
721 CGGCACGGGCATCCTGTGTGCGGCCCGCATGGAGGGTTTGAAAAGTTCACGGAGGCTCC 780
781 CTGAGGAGCCTCTCAGATCGGCTGCTGCGGGTGCAGGGCGTGA CTACCGCTGGGTGCTT 840
841 GCCAAAGAGATAGGGACGCATATGCTTTTTAAAGCAATCTAAAAATAATAAAGTATAG 900
901 CGACTATATACCTACTTTTAAATCAACTGTTTTGAATAGAGGCAGAGCTATTTTATATT 960
961 ATCAAATGAGAGCTACTCTGTTACATTTCTTAACATATAAACATCGTTTTTTACTTCTTC 1020
1021 TGGTAGAATTTTTTAAAGCATAATTGGAATCCTTGGATAAATTTTGTAGCTGGTACACTC 1080
1081 TGGCCTGGGTCTCTGAATTCAGCCTGTCACCGATGGCTGACTGATGAAATGGACACGTCT 1140
1141 CATCTGACCCACTCTTCCTTCCACTGAAGGTCTTCACGGGCCTCCAGGTGGACCAAAGGG 1200
1201 ATGCACAGGCGGCTCGCATGCCCCAGGGCCAGCTAAGAGTTCCAAAGATCTCAGATTTGG 1260
1261 TTTTAGTCATGAATACATAAACAGTCTCAAACGCGACAATTTTTTCCCCCTTTTGAAAG 1320
1321 CCACTGGGGCCAATTTGTGGTTAAGAGGTGGTGAGATAAGAAGTGAACGTGACATCTTT 1380
1381 GCCAGTTGTGAGAAGAATCCAAGCAGGTATTGGCTTAGTTGTAAGGGCTTTAGGATCAGG 1440
1441 CTGAATATGAGGACAAAGTGGGCCACGTTAGCATCTGCAGAGATCAATCTGGAGGCTTCT 1500
1501 GTTTCTGCATTCTGCCACGAGAGCTAGGTCCTTGATCTTTTCTTTAGATTGAAAGTCTGT 1560
1561 CTCTGAACACAATTATTTGTAAAAGTTAGTAGTTCTTTTTTAAATCATTAAAAGAGGCTT 1620
1621 GCTGAAAAAAAAAAAAAAAAAAAA 1642

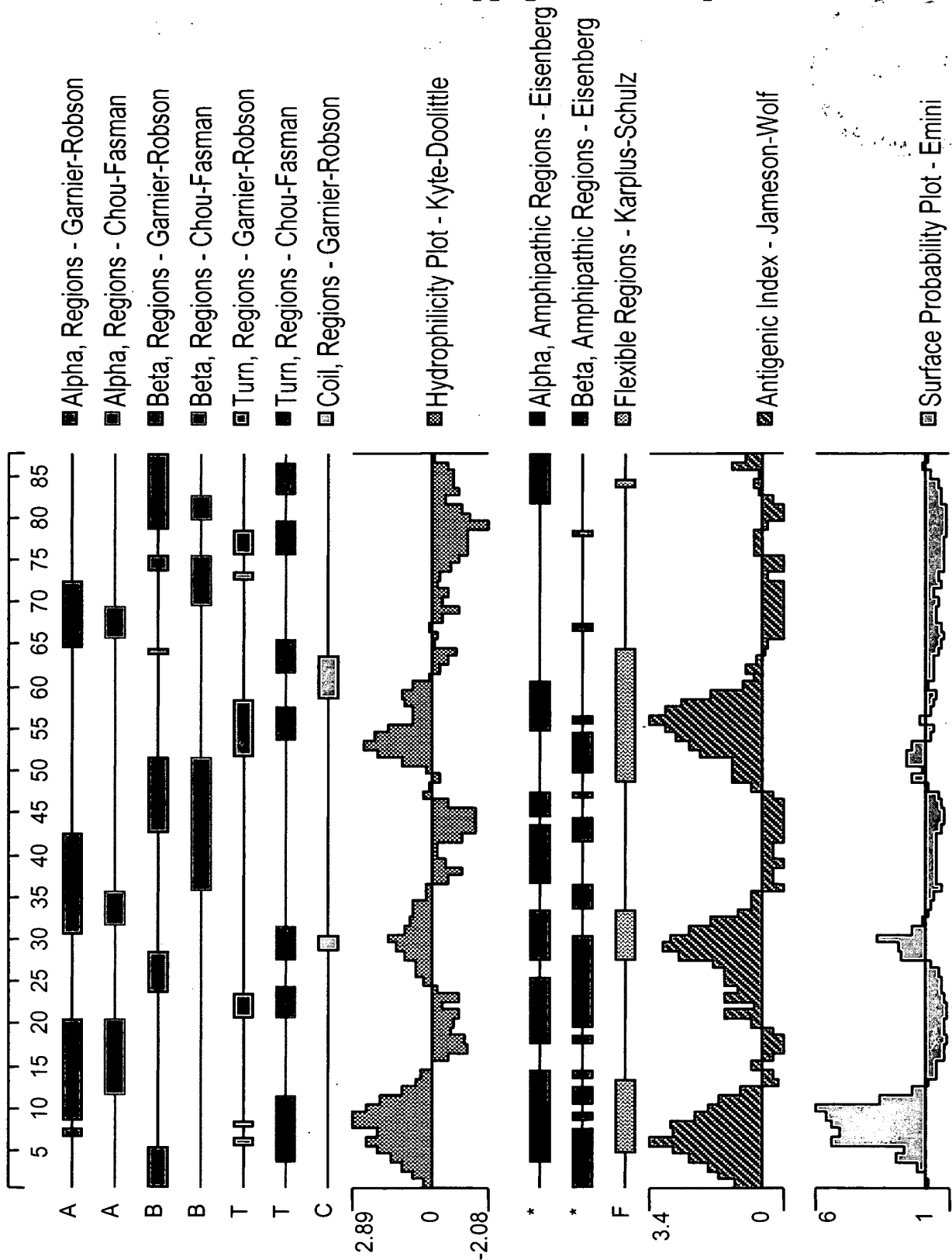
FIG. 2B

	160	170	180	190	200
109	H M N S V P I Q Q E I L V L R R E P - - - - - P H C P N S F R L E K I L - - V S V G C T C V T P II-17.aa				
112	H M N S V L I Q Q E I L V L K R E P - - - - - E S C P F T F R V E K M L - - V G V G C T C V A S mII-17.aa				
105	H M N S V P I Q Q E I L V V R K G H - - - - - Q P C P N S F R L E K M L - - V T V G C T C V T P vII-17.aa				
137	S M V S V P V F - S Q V P V R R R L C P P P P R T G P C R Q - - - R A V M E T I A V G C T C I - - II20.aa				
35	A L N S V R L L Q S L L V L R R R P C S R D G S G L P T P G A F A F H T E F I H V P V G C T C V - - II-21.aa				
145	A L N S V R L L Q S L L V L R R R P C S R D G S G L P T P G A F A F H T E F I H V P V G C T C V - - II21FL.aa				
88	R F R S A P V Y M P T V V L R R T P A C A G R S V - - - - - Y T E A Y V T I P V G C T C V P E II-22.aa				
101	R F R S A P V Y M P T V V L R R T P A C A G R S V - - - - - Y T E A Y V T I P V G C T C V P E II22ext.aa				

	210	220	230
150	IVHHVA		
153	IVRQAA		
146	IVHNV D		
180	- - - - -	- - - - -	- - - - - F
83	- - - - -	- - - - -	- - - - - L PRSV
193	- - - - -	- - - - -	- - - - - L PRSV
131	PEKDAD	SINSSIDKQGAKLL	LGPNDAPAGP
144	PEKDAD	SINSSIDKQGAKLL	LGPNDAPAGP

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Interleukin-21 Polypeptide Analysis



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Interleukin-22 Polypeptide Analysis

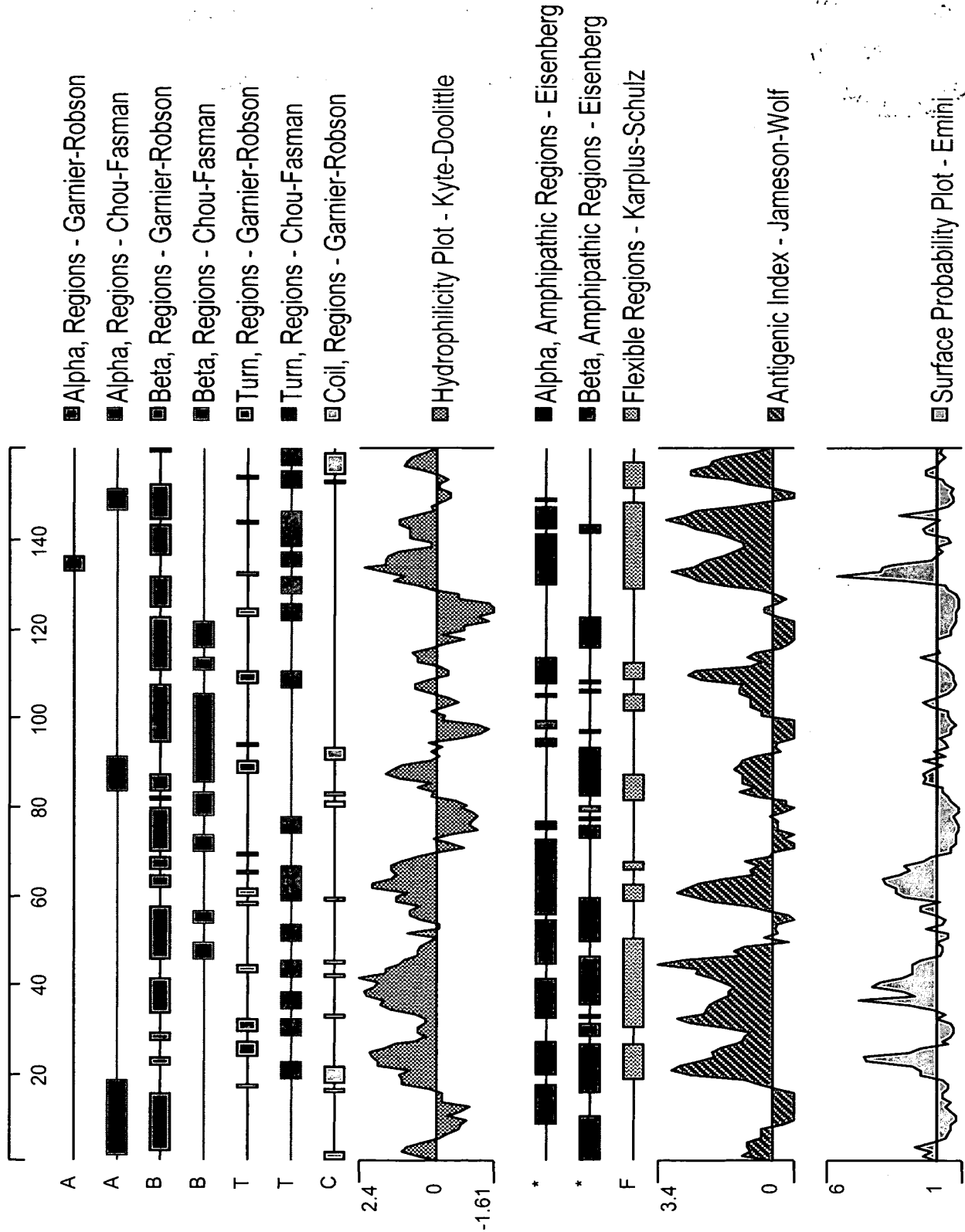


FIG. 5

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Interleukin-21

1	GCTCCAAGCCCAGCCTGCCCCGCTGCCGCCACCATGACGCTCCTCCCCGGCCTCCTGTTT	60
1	<u>M T L L P G L L F</u>	9
61	CTGACCTGGCTGCACACATGCCTGGCCCACCATGACCCCTCCCTCAGGGGGCACCCCCAC	120
10	<u>L T W L H T C L A</u> H H D P S L R G H P H	29
121	AGTCACGGTACCCACACTGCTACTCGGCTGAGGAACTGCCCTCGGCCAGGCCCCCCCCA	180
30	S H G T <u>P H C Y S A E</u> E L P L G Q A P P	49
	<i>Domain V</i>	
181	CACCTGCTGGCTCGAGGTGCCAAGTGGGGGAGGCTTTGCCTGTAGCCCTGGTGTCCAGC	240
50	H L L A R G A K W G Q A L <u>P V A L V S S</u>	69
	<i>Domain VI</i>	
241	CTGGAGGCAGCAAGCCACAGGGGGAGGCACGAGAGGCCCTCAGCTACGACCCAGTGCCCCG	300
70	L E A A S H R G R H E R P S A T T Q C P	89
301	GTGCTGCGGCCGAGGAGGTGTTGGAGGCAGACACCCACCAGCGCTCCATCTCACCCCTGG	360
90	V L R P E E V L E A D T H Q <u>R S I S P W</u>	109
	<i>Domain VII</i>	
361	AGATACCGGGTGGACACGGATGAGGACCGCTATCCACAGAAGCTGGCCTTCGCCGAGTGC	420
110	R Y R <u>V D T D E D R Y P</u> Q K L A F A E <u>C</u>	129
	<i>Domain I</i> <i>Domain II</i>	
421	CTGTGCAGAGGCTGTATCGATGCACGGACGGGCCGCGAGACAGCTGCGCTCAACTCCGTG	480
130	<u>L C R G C</u> I D A R T G R E T A A L N S V	149
	<i>Domain II</i>	
481	CGGCTGCTCCAGAGCCTGCTGGTGCTGCGCCGCCGGCCCTGCTCCCGCGACGGCTCGGGG	540
150	R L L Q S L <u>L V L R R R P</u> C S R D G S G	169
	<i>Domain III</i>	
541	CTCCCCACACCTGGGGCCTTTGCCTTCCACACCGAGTTCATCCACGTCCCCGTGCGCTGC	600
170	L P T P G A F A F H T E F I H <u>V P V G C</u>	189
	<i>Domain IV</i>	

FIG. 6A

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Interleukin-21

601 ACCTGCGTGCTGCCCCGTTCA GTGTGACCGCCAAGGCCGTGGGGCCCTTAGACTGGACAC 660
190 T C V L P R S V 197
Domain IV
661 GTGTGCTCCCCAGAGGGCACCCCCTATTTATGTGTATTTATTGTTATTTATATGCCTCCC 720
721 CCAACACTACCCTTGGGGTCTGGGCATTCCCCGTGTCTGGAGGACAGCCCCCACTGTTC 780
781 TCCTCATCTCCAGCCTCAGTAGTTGGGGGTWGAAGGAGCTCAGCACCTCTCCAGCCCTT 840
841 AAAGCTGCAGAAAAGGTGTCACACGGCTGCCTGTACCTTGGYTCCCTGTCCTGCTCCCGG 900
901 CTTCCCTTACCCTATCACTGGCCTCAGGCCCCCGCAGGCTGCCTCTTCCCAACCTCCTTG 960
961 GAAGTACCCCTGTTTCTTAAACAATTATTTAAGTGTACGTGTATTATTAAACTGATGAAC 1020
1021 ACAA 1067

FIG. 6B

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Interleukin-21 Polypeptide Analysis

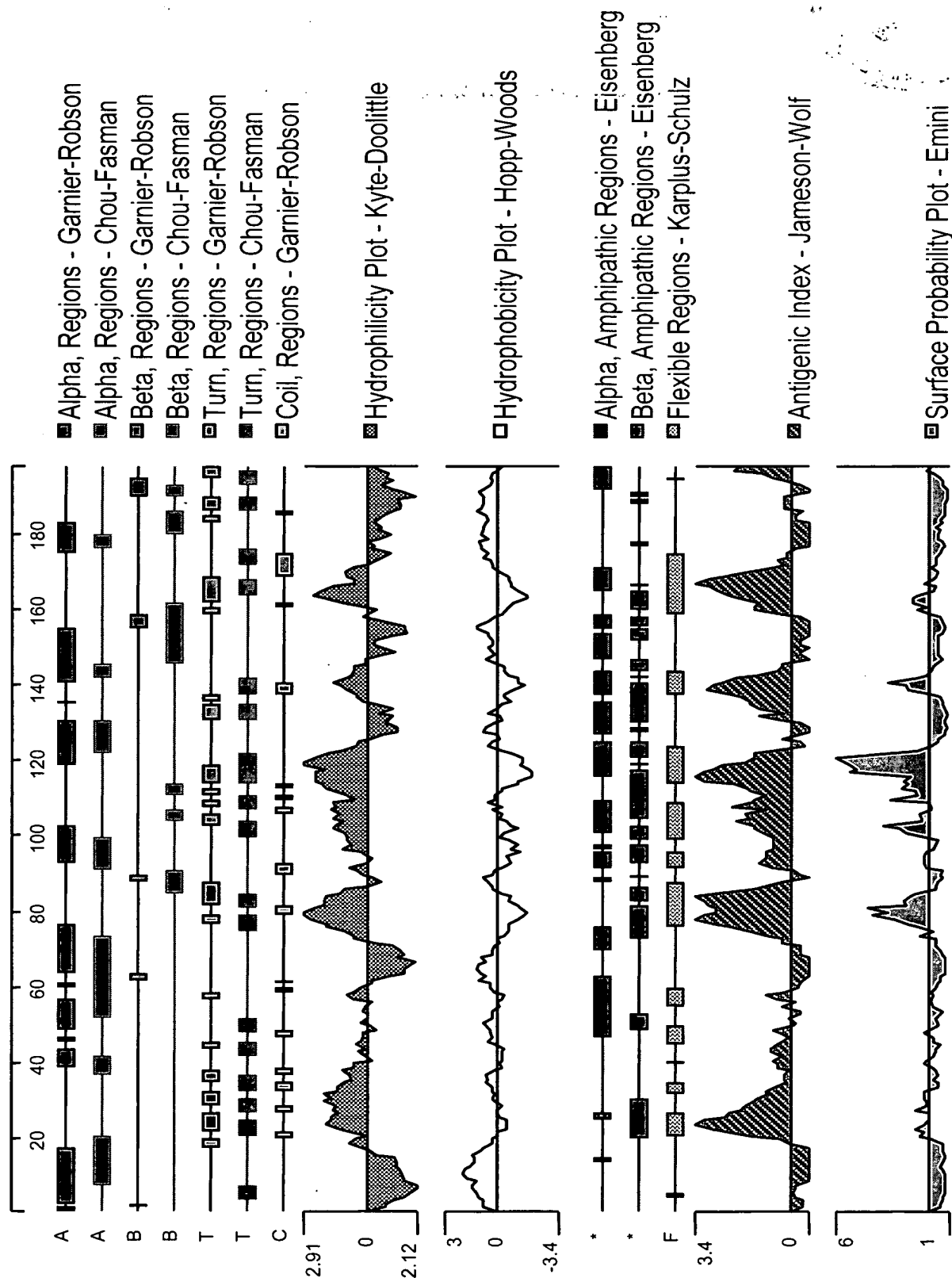


FIG. 7

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Interleukin-22

1 GGCTGCGCGGACCGGCCGGAGGAGCTACTGGAGCAGCTGTACGGGCGCCTGGCGGCCGGC 60
 1 G C A D R P E E L L E Q L Y G R L A A G 20
 CD-VI
 #
 61 GTGCTCAGTGCCTTCCACCACAGCTGCAGCTGGGGCCGCGTGAGCAGGCGCGCAACGCG 120
 21 V L S A F H H T L Q L G P R E Q A R N A 40
 CD-VI
 121 AGCTGCCCCGAGGGGGCAGGCCCCGCCACCGCCGCTTCCGGCCGCCACCAACCTGCGC 180
 41 S C P A G G R P A D R R F R P P T N L R 60
 181 AGCGTGTGCGCCCTGGGCCTACAGAATCTCCTACGACCCGCGAGGTACCCCAGGTACCTG 240
 61 S V S P W A Y R I S Y D P A R Y P R Y L 80
 CD-VII CD-I
 241 CCTGAAGCCTACTGCCTGTGCCGGGGCTGCCTGACCGGGCTGTTCCGGCAGGAGGACGTG 300
 81 P E A Y C L C R G C L T G L F G E E D V 100
 CD-II
 301 CGCTTCCGCAGCGCCCCTGTCTACATGCCCACCGTCGTCTGCGCCGCACCCCCGCCTGC 360
 101 R F R S A P V Y M P T V V L R R T P A C 120
 CD-III
 361 GCCGGCGGCCGTTCCGTCTACACCGAGGCCTACGTCACCATCCCCGTGGGCTGCACCTGC 420
 121 A G G R S V Y T E A Y V T I P V G C T C 140
 CD-IV
 #
 421 GTCCCCGAGCCGAGAAGGACGCAGACAGCATCAACTCCAGCATCGACAAACAGGGCGCC 480
 141 V P E P E K D A D S I N S S I D K Q G A 160
 CD-IV
 481 AAGCTCCTGCTGGGCCCCAACGACGCGCCCGCTGGCCCTGA 522
 161 K L L L G P N D A P A G P 174

FIG. 8

Interleukin-22 Polypeptide Analysis

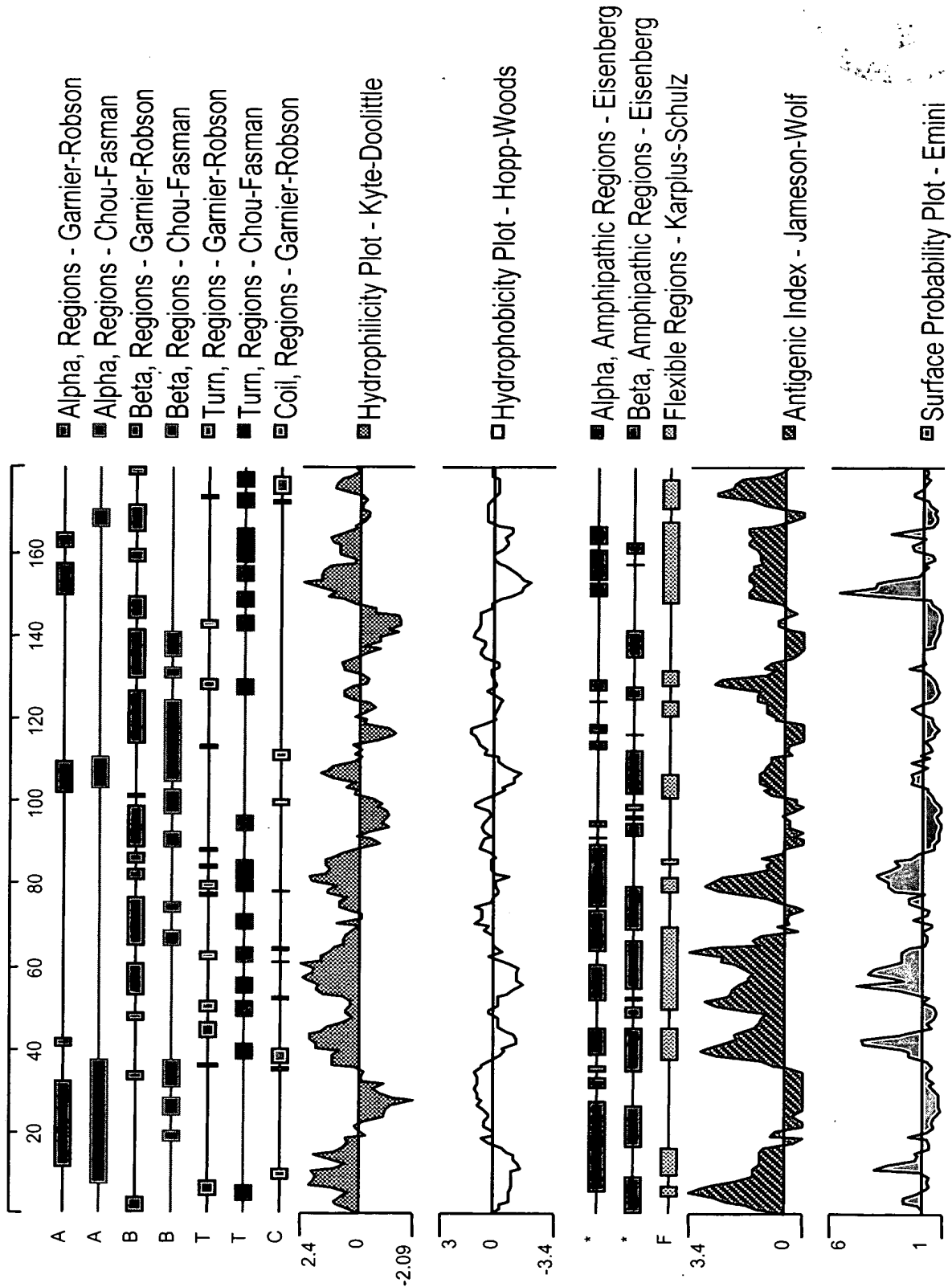


FIG. 9